

## SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Michael A. Apicella  
Melvin G. Sunshine  
Na-Gyong Lee  
Bradley Gibson  
Rasappa Arumugham

10 (ii) TITLE OF INVENTION: Non-Toxic Mutants of Pathogenic Gram-Negative Bacteria

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear

(B) STREET: 1800 One M&T Plaza

(C) CITY: Buffalo

(D) STATE: New York

20 (E) COUNTRY: United States

(F) ZIP: 14203-2391

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1

(D) SOFTWARE: Wordperfect for Windows 5.1

25 (vi) APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Nelson, M. Bud

(B) REGISTRATION NUMBER: 35,300

30 (C) REFERENCE DOCKET NUMBER: 22244.0002

(viii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (716) 856-4000

(B) TELEFAX: (716) 849-0349

40 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 969 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double-stranded

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: yes

(iv) ORIGINAL SOURCE:

(A) ORGANISM: *H. influenzae*

50 (B) STRAIN: 2019

(C) CELL TYPE: bacterium

(v) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAAACTACGC CCCTAACTTA CGTGGAAAGA ACA ATG AAA AAC 42

		Met	Lys	Asn
		1		
5	GAA AAA CTC CCT CAA TTT CAA CCG CAC TTT TTA GCC CCA 81			
	Glu Lys Leu Pro Gln Phe Gln Pro His Phe Leu Ala Pro	5	10	15
10	AAA TAC TGG CTT TTT TGG CTA GGC GTG GCA ATT TGG CGA 120			
	Lys Tyr Trp Leu Phe Trp Leu Gly Val Ala Ile Trp Arg	20	25	
15	AGT ATT TTA TGT CTT CCC TAT CCT ATT TTG CGC CAT ATT 159			
	Ser Ile Leu Cys Leu Pro Tyr Pro Ile Leu Arg His Ile	30	35	40
20	GGT CAT GGT TTC GGT TGG CTG TTT TCA CAT TTA AAA GTG 198			
	Gly His Gly Phe Gly Trp Leu Phe Ser His Leu Lys Val	45	50	55
25	GGT AAA CGT CGA GCT GCC ATT GCA CGC CGT AAT CTT GAA 237			
	Gly Lys Arg Arg Ala Ala Ile Ala Arg Arg Asn Leu Glu	60	65	
30	CTT TGT TTC CCT GAT ATG CCT GAA AAC GAA CGT GAG ACG 276			
	Leu Cys Phe Pro Asp Met Pro Glu Asn Glu Arg Glu Thr	70	75	80
35	ATT TTG CAA GAA AAT CTT CGT TCA GTA GGC ATG GCA ATT 315			
	Ile Leu Gln Glu Asn Leu Arg Ser Val Gly Met Ala Ile	85	90	95
40	ATC GAA ACT GGC ATG GCT TGG TTT TGG TCG GAT TCA CGT 354			
	Ile Glu Thr Gly Met Ala Trp Phe Trp Ser Asp Ser Arg	100		105
45	ATC AAA AAA TGG TCG AAA GTT GAA GGC TTA CAT TAT CTA 393			
	Ile Lys Lys Trp Ser Lys Val Glu Gly Leu His Tyr Leu	110	115	120
50	AAA GAA AAT CAA AAA GAT GGA ATT GTT CTC GTC GGC GTT 432			
	Lys Glu Asn Gln Lys Asp Gly Ile Val Leu Val Gly Val	125		130
55	CAT TTC TTA ACG CTA GAA CTT GGC GCA CGC ATC ATT GGT 471			
	His Phe Leu Thr Leu Glu Leu Gly Ala Arg Ile Ile Gly	135	140	145
60	TTA CAT CAT CCT GGC ATT GGT GTT TAT CGT CCA AAT GAT 510			
	Leu His His Pro Gly Ile Gly Val Tyr Arg Pro Asn Asp	150	155	
65	AAT CCT TTG CTT GAT TGG CTA CAA ACA CAA GGC CGT TTA 549			
	Asn Pro Leu Pro Asp Trp Leu Gln Thr Gln Gly Arg Leu	160	165	170

CGC TCC AAT AAA GAT ATG CTT GAT CGT AAA GAT TTA CGC 588  
 Arg Ser Asn Lys Asp Met Leu Asp Arg Lys Asp Leu Arg  
 175 180 185

5 GGA ATG ATC AAA GCT TTA CGC CAC GAA GAA ACC ATT TGG 627  
 Gly Met Ile Lys Ala Leu Arg His Glu Glu Thr Ile Trp  
 190 195

10 TAT GCG CCT GAT CAC GAT TAC GGC AGA AAA AAT GCC GTT 666  
 Tyr Ala Pro Asp His Asp Tyr Gly Arg Lys Asn Ala Val  
 200 205 210

15 TTT GTT CCT TTT TTT GCA GTA CCT GAC ACT TGC ACT ACT 705  
 Phe Val Pro Phe Phe Ala Val Pro Asp Thr Cys Thr Thr  
 215 220

20 ACT GGT AGT TAT TAT TTA TTG AAA TCC TCG CAA AAC AGC 744  
 Thr Gly Ser Tyr Tyr Leu Leu Lys Ser Ser Gln Asn Ser  
 225 230 235

25 AAA GTG ATT CCA TTT GCG CCA TTA CGC AAT AAA GAT GGT 783  
 Lys Val Ile Pro Phe Ala Pro Leu Arg Asn Lys Asp Gly  
 240 245 250

30 TCA GGC TAT ACC GTG AGC ATT TCA GCG CCT GTT GAT TTT 822  
 Ser Gly Tyr Thr Val Ser Ile Ser Ala Pro Val Asp Phe  
 255 260

35 ACA GAT TTA CAA GAT GAA GTA GCG ATA GCT GTG CGA ATG 861  
 Thr Asp Leu Gln Asp Glu Val Ala Ile Ala Val Arg Met  
 265 270 275

40 AAT CAA ATC GTT GAA AAG GAA ATC ATG AAG GGC ATA TCA 900  
 Asn Gln Ile Val Glu Lys Glu Ile Met Lys Gly Ile Ser  
 280 285

45 CAA TAT ATG TGG CTA CAT CGT CGT TTT AAA ACA CGC CCC  
 Gln Tyr Met Trp Leu His Arg Arg Phe Lys Thr Arg Pro  
 290 295 300

50 GAT GAA AAT ACG CCT AGT TTA TAC GAT TAA 969  
 Asp Glu Asn Thr Pro Ser Leu Tyr Asp  
 305 310

(3) INFORMATION FOR SEQ ID NO:2:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 nucleotides  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single-stranded  
 (D) TOPOLOGY: linear  
 (ii) ORIGINAL SOURCE:  
 (A) ORGANISM: *H. influenzae*  
 (B) STRAIN: 2019

(iii) IMMEDIATE SOURCE: synthesized  
(iv) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCAATATGGC GCAAAATAGG ATAGGGAAGA C 31

5

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 nucleotides

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single-stranded  
(D) TOPOLOGY: linear

(ii) ORIGINAL SOURCE:

(A) ORGANISM: *H. influenzae*

(iii) FEATURE:

15 (A) OTHER INFORMATION: uptake sequence for  
transformation

(iv) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGTGCAGT 9

20

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 nucleotides

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single-stranded  
(D) TOPOLOGY: linear

(ii) FEATURE:

(A) OTHER INFORMATION: hybridizes to TNF $\alpha$  mRNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30

ATCTCTCAGC TCCACGCCAT TGGCCAGGAG 30

(6) INFORMATION FOR SEQ ID NO:5:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single-stranded

(D) TOPOLOGY: linear

(ii) FEATURE:

40 (A) OTHER INFORMATION: does not hybridize to TNF $\alpha$   
mRNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCCTGGCCA ATGGCGTGGA GCTGAGAGAT 30